GenSSI: a new toolbox for testing structural identifiability insystems biology

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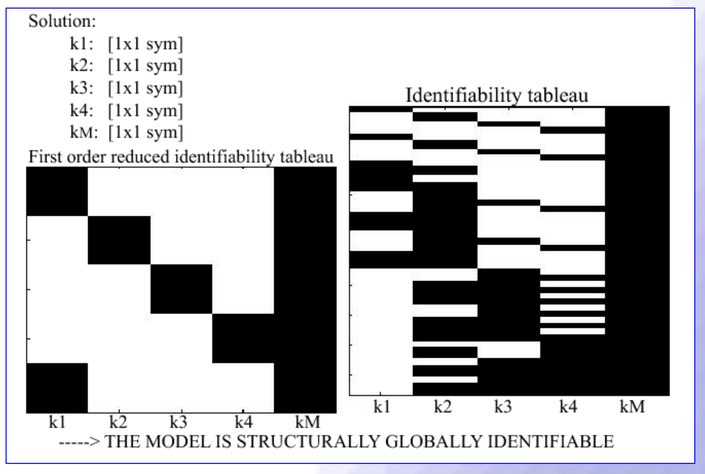
The background:

- the problem of parameter estimation has many possible pitfalls;
- many difficulties arrise because of the unchecked structural identifiability;

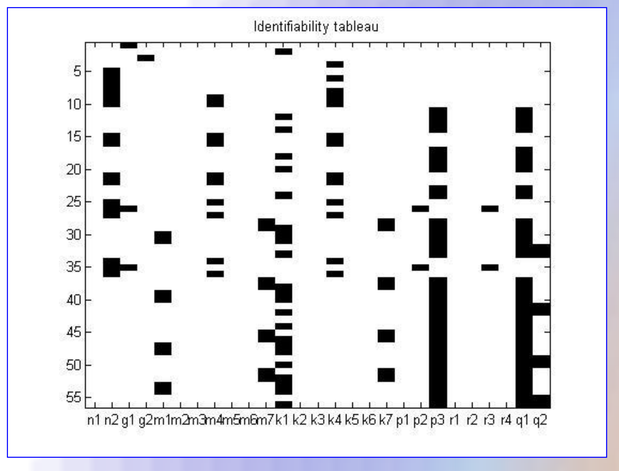
The formulation:



- structural identifiability studies the uniqueness of the estimated parameters;
- unique solution of the parameters will guarantee the **structural global identifiability**;
- more than one solution gives the **structural local identifiability** of the parameters;
- the model is **structurally non-identiafiable** if no solution of the parameters can be found;

The toolbox:

- GenSSI is based on generating series approach;
- it uses identifiability tableau;
- performs several steps of symbolic computations;
- represents figures describing the structural identifiability;
- displays the structural identifiability result.

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*********************************************************************
 -----> THE MODEL IS STRUCTURALLY NON-IDENTIFIABLE
*********************************************************************
        The structurally globally identifiable parameters are:
        [  g1   k1   k4   n2   m4 ]

        The structurally locally identifiable parameters are:
        [ g2 ]

        The structurally non-identifiable parameters are:
        [ r4   r2   r1   p1   k6   k5   k3   k2   m6   m5   m3   m2   n1 ]
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References:

[1] Chis, O., Banga, J. R., Balsa-Canto, E. *GenSSI: a software toolbox for structural identifiability analysis of biological models* (sent for publication).

[2] Balsa-Canto, E., Alonso, A., and Banga, J. (2010). *An iterative identification procedure for dynamic modeling of biochemical networks. BMC Systems Biology, 4(1), 11.*

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